

What is claimed is:

1. A recombinant nucleic acid molecule comprising as operably linked components:
(A) a promoter that functions in a plant cell to cause production of an mRNA molecule; and
(B) a nucleic acid sequence that has at least 85% identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, complements thereof, and fragments of either.
2. The recombinant nucleic acid molecule of claim 1, wherein the promoter is a seed-specific promoter.
3. The recombinant nucleic acid molecule of claim 2, wherein the promoter is a 7S promoter.
4. The recombinant nucleic acid molecule of claim 1, wherein the nucleic acid sequence is in a sense orientation relative to the promoter.
5. The recombinant nucleic acid molecule of claim 1, wherein the nucleic acid sequence is in an antisense orientation relative to the promoter.
6. The recombinant nucleic acid molecule of claim 1, wherein the nucleic acid sequence is capable of expressing a dsRNA.
7. The recombinant nucleic acid molecule of claim 1, wherein said nucleic acid molecule further comprises one or more additional nucleic acid sequences, wherein said additional nucleic acid sequences encode an enzyme selected from the group consisting of beta-ketoacyl-ACP synthase I, beta-ketoacyl-ACP synthase IV, and delta-9 desaturase.
8. The recombinant nucleic acid molecule of claim 7, wherein the additional nucleic acid sequence encodes beta-ketoacyl-ACP synthase IV.
9. The recombinant nucleic acid molecule of claim 7, wherein the additional nucleic acid sequences encode beta-ketoacyl-ACP synthase IV and delta-9 desaturase.

10. An intron obtained from a genomic polynucleotide sequence wherein said genomic polynucleotide sequence is selected from the group consisting of:

- a) a genomic polynucleotide sequence having at least 70% identity to coding regions of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;
- b) a genomic polynucleotide sequence having at least 80% identity to coding regions of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1;
- c) a genomic polynucleotide sequence having at least 90% identity to coding regions of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1; and
- d) a genomic polynucleotide sequence having at least 95% identity to coding regions of SEQ ID NO: 1 over the entire length of SEQ ID NO: 1.

11. An intron obtained from a genomic polynucleotide sequence wherein said genomic polynucleotide sequence is selected from the group consisting of:

- a) a genomic polynucleotide sequence having at least 70% identity to coding regions of SEQ ID NO: 10 over the entire length of SEQ ID NO: 10;
- b) a genomic polynucleotide sequence having at least 80% identity to coding regions of SEQ ID NO: 10 over the entire length of SEQ ID NO: 10;
- c) a genomic polynucleotide sequence having at least 90% identity to coding regions of SEQ ID NO: 10 over the entire length of SEQ ID NO: 10; and
- d) a genomic polynucleotide sequence having at least 95% identity to coding regions of SEQ ID NO: 10 over the entire length of SEQ ID NO: 10.

12. A transformed soybean plant comprising a recombinant nucleic acid molecule, the recombinant nucleic acid molecule comprising as operably linked components: (A) a promoter that functions in a plant to cause production of an mRNA molecule; and (B) a nucleic acid sequence that has at least 85% identity to a nucleic acid sequence selected from the group

consisting of SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, complements thereof, and fragments of either.

13. The transformed plant of claim 12, wherein said transformed plant exhibits a reduced palmitic acid level relative to a plant with a similar genetic background but lacking the recombinant nucleic acid molecule.

14. The transformed plant of claim 12, wherein said transformed plant produces a seed with a reduced palmitic acid level relative to a plant with a similar genetic background but lacking the recombinant nucleic acid molecule.

15. The transformed plant of claim 12, wherein said transformed plant exhibits a reduced stearic acid level relative to a plant with a similar genetic background but lacking the recombinant nucleic acid molecule.

16. The transformed plant of claim 12, wherein said transformed plant produces a seed with a reduced stearic acid level relative to a plant with a similar genetic background but lacking the recombinant nucleic acid molecule.

17. The transformed plant of claim 12, wherein said transformed plant produces a seed with a reduced saturated fatty acid content relative to a plant with a similar genetic background but lacking the recombinant nucleic acid molecule.

18. The transformed plant of claim 12, wherein said transformed plant exhibits an increased oleic acid level relative to a plant with a similar genetic background but lacking the recombinant nucleic acid molecule.

19. The transformed plant of claim 12, wherein said transformed plant produces a seed with an increased oleic acid level relative to a plant with a similar genetic background but lacking the recombinant nucleic acid molecule.

20. A transformed soybean plant having a nucleic acid molecule that comprises (a) a first promoter operably linked to a first nucleic acid molecule having a first nucleic acid sequence that has 85% or greater identity to a nucleic acid sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6,

SEQ ID NO: 7, SEQ ID NO: 8, complements thereof, and fragments of either, and (b) a second nucleic acid molecule with a second nucleic acid sequence that encodes an enzyme selected from the group consisting of beta-ketoacyl-ACP synthase I, beta-ketoacyl-ACP synthase IV, and delta-9 desaturase.

21. The transformed soybean plant according to claim 20, wherein the first promoter is a seed specific promoter.

22. The transformed soybean plant according to claim 20, wherein the first promoter is a 7S promoter.

23. The transformed soybean plant according to claim 20, wherein said first nucleic acid molecule is transcribed and is capable of at least partially reducing the level of a transcript encoded by an endogenous *FATB* gene.

24. A method of modifying the lipid composition in a host cell comprising: transforming a host cell with a DNA construct comprising as operably associated components in the 5' to 3' direction of transcription, a transcriptional initiation region functional in said host cell, a DNA sequence selected from the group consisting of SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, complements thereof, and fragments of either, and a transcription termination sequence, and growing said cell under conditions wherein transcription of said DNA sequence is initiated, whereby said lipid composition is modified.